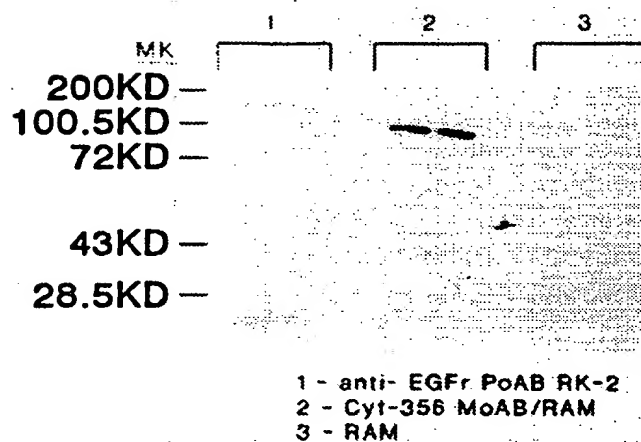


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FIGURE 1



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FIGURE 2A

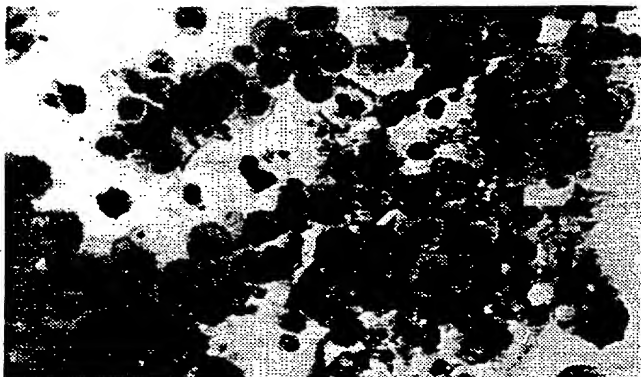


FIGURE 2B

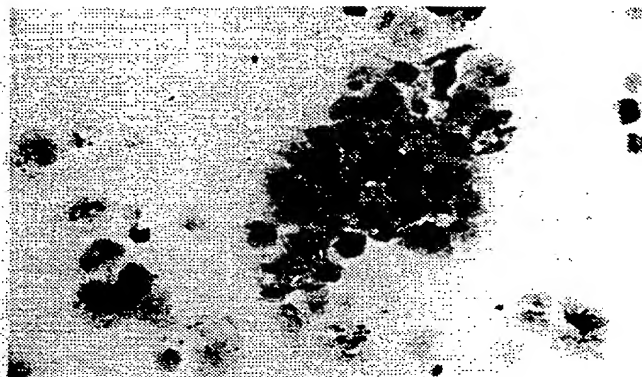


FIGURE 2C

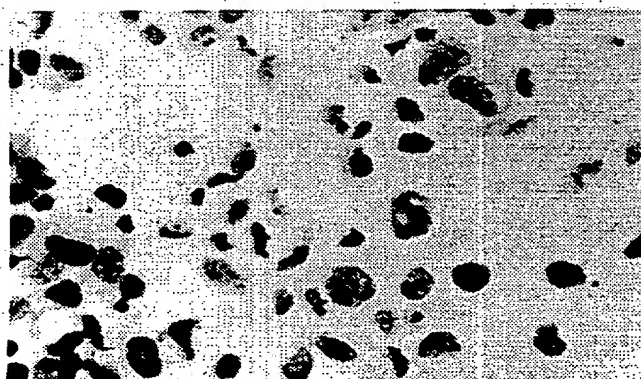
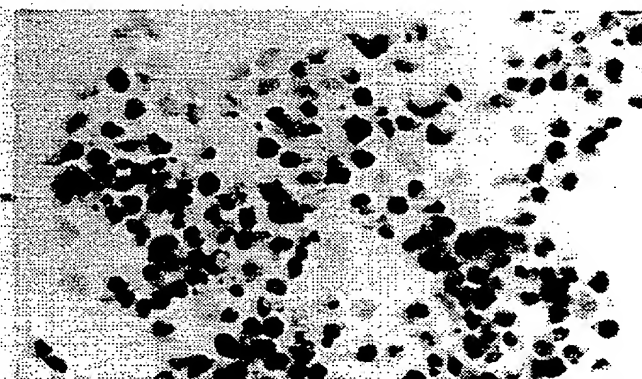


FIGURE 2D



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FIGURE 3A

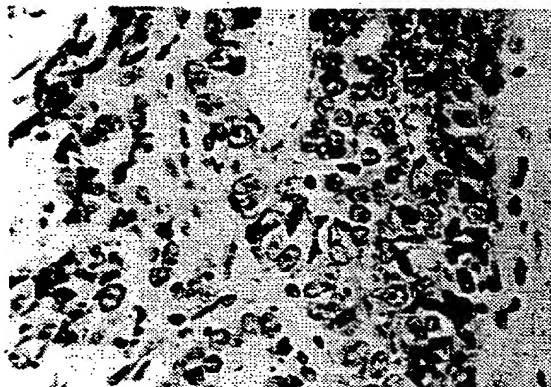


FIGURE 3B

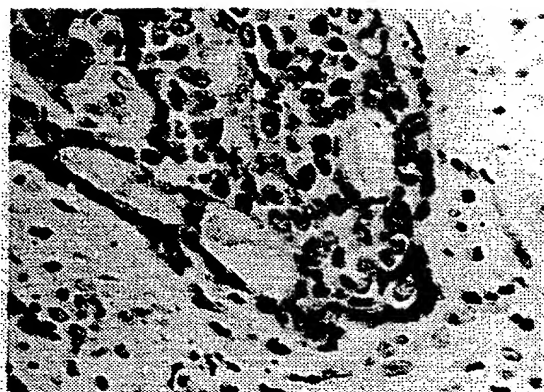


FIGURE 3C

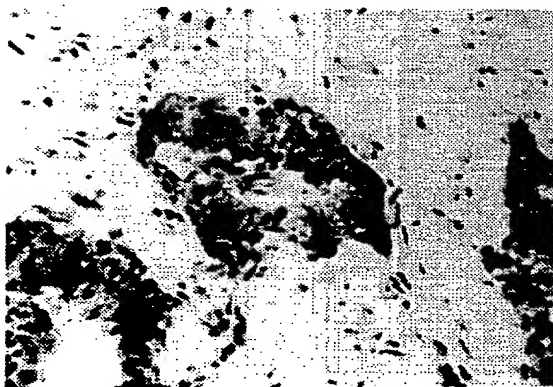
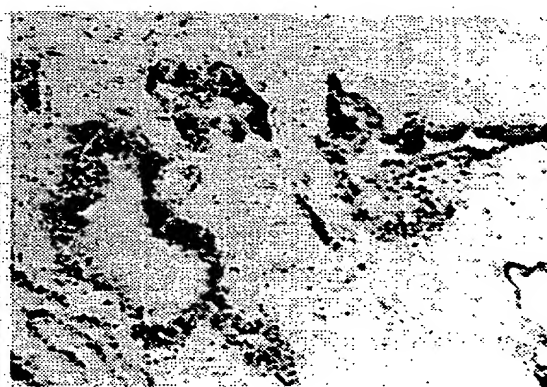
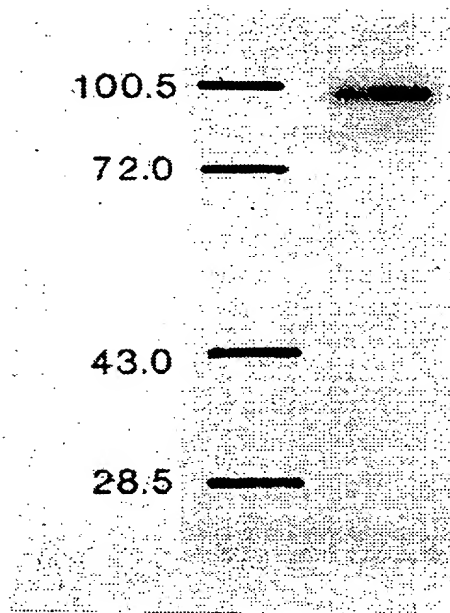


FIGURE 3D



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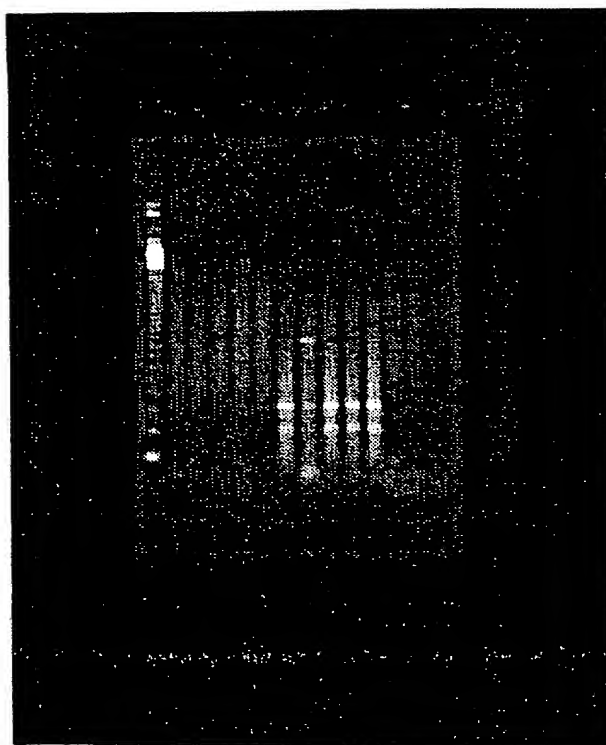
FIGURE 4



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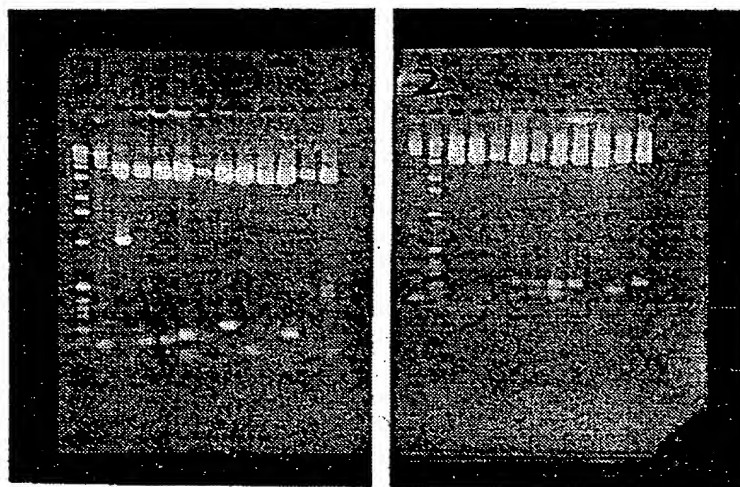
FIGURE 5



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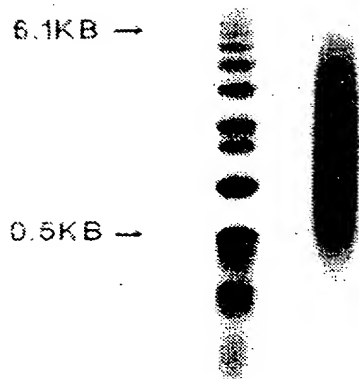
FIGURE 6A FIGURE 6B



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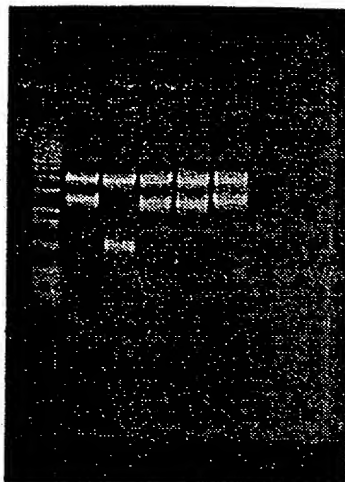
FIGURE 7



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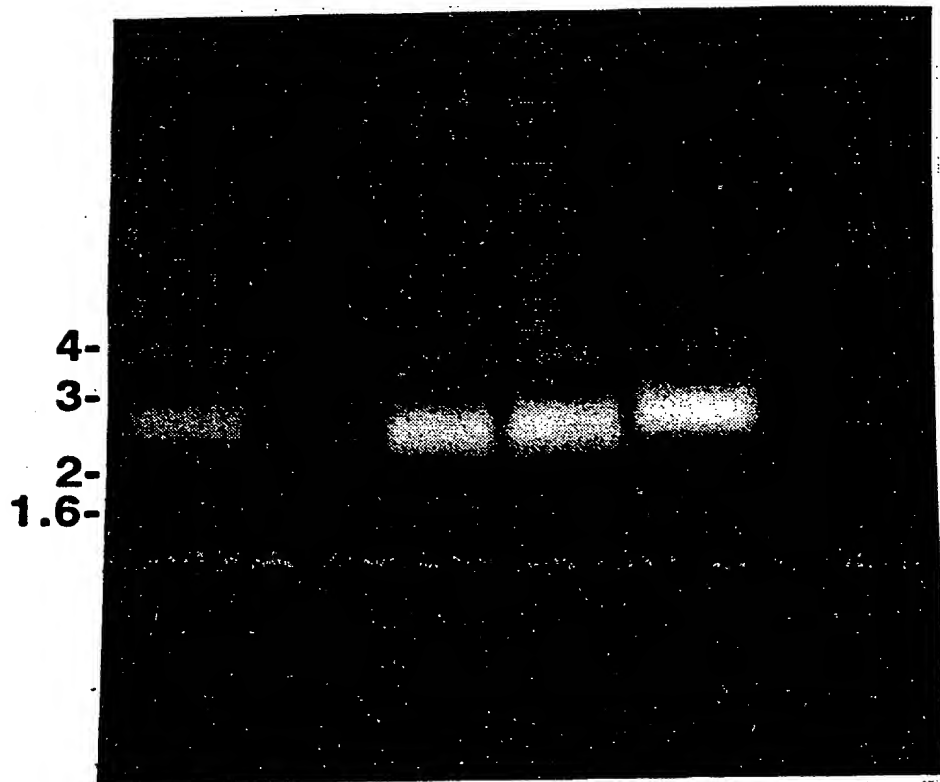
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FIGURE 8



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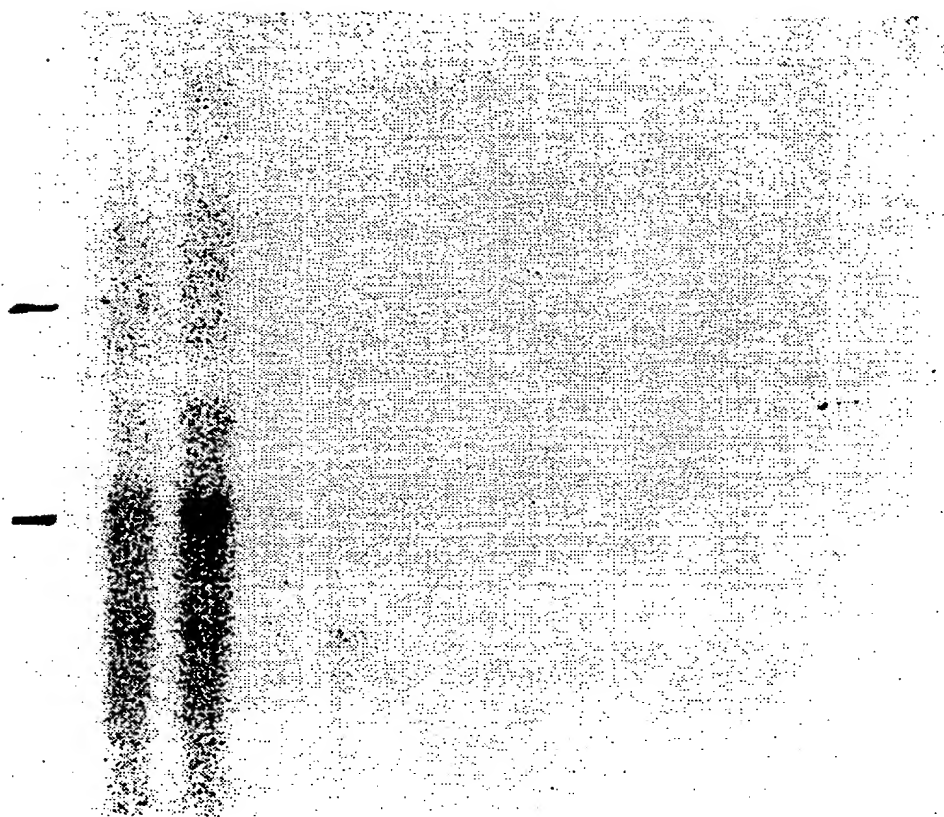
FIGURE 9



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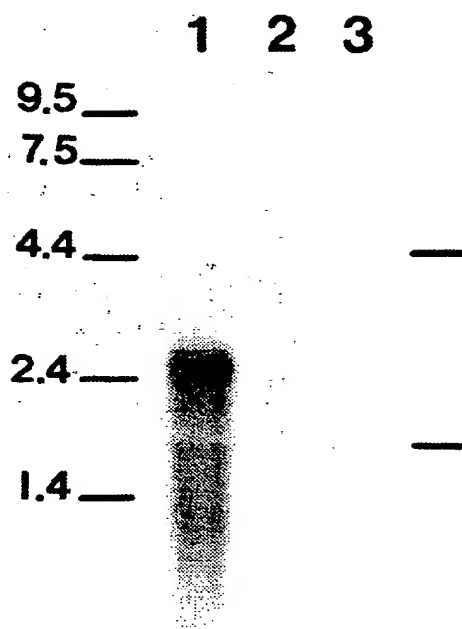
FIGURE 10



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FIGURE 11



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FIGURE 12A

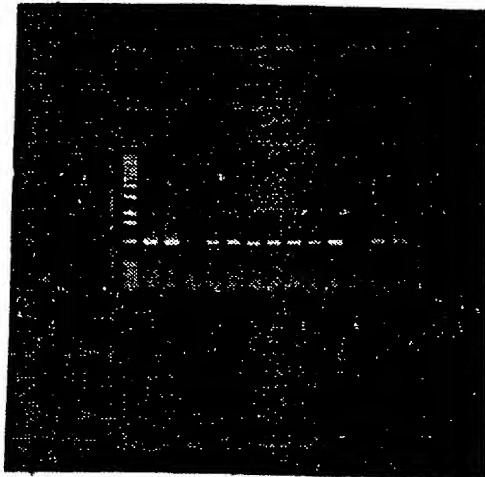
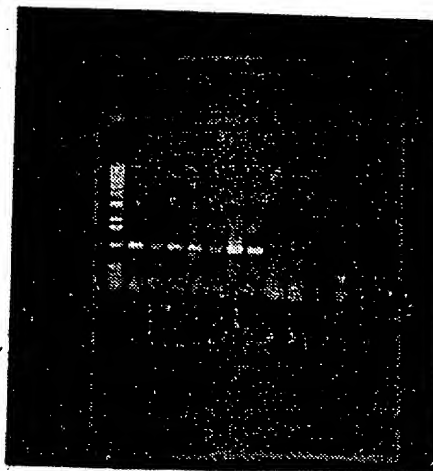
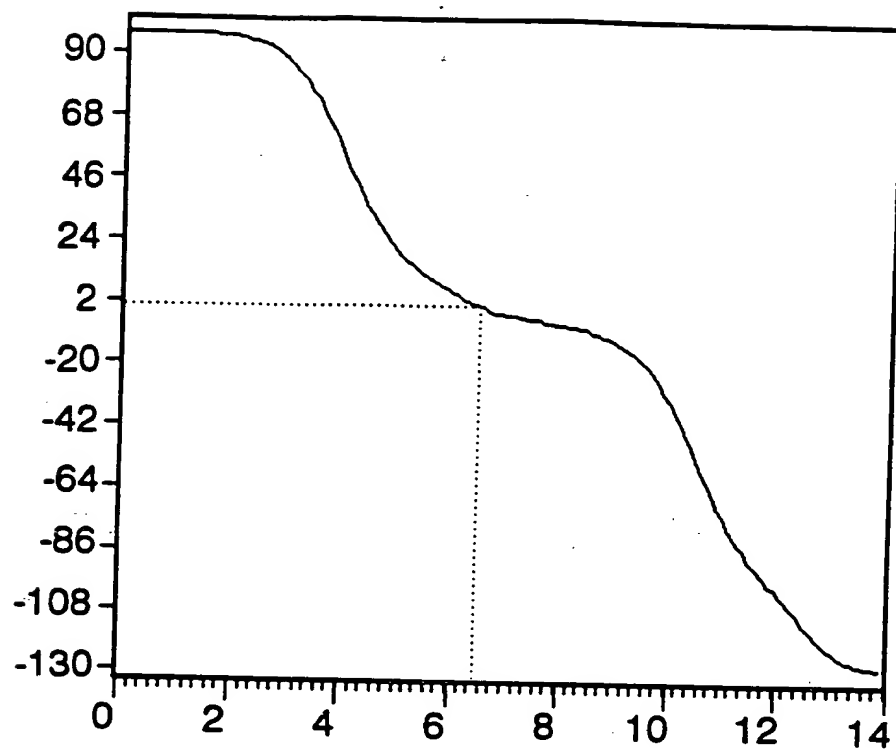


FIGURE 12B



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FIGURE 13



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FIGURE 14-2

91	H	H	H	H	E	H	C	E	E	E	T	C	H	H	H	H	H	H	H	H	H	E	E	E	E	T
121	T	T	C	C	E	E	E	E	E	E	C	T	C	H	E	E	E	E	T	T	C	C	C	C	T	T
151	T	E	E	E	E	E	E	E	E	E	T	E	C	C	T	C	C	C	E	E	E	E	E	E	E	H
181	H	H	H	H	H	H	H	H	H	H	H	H	T	T	T	E	E	E	E	E	E	E	E	E	E	E
211	T	T	C	C	H	H	H	H	H	H	E	E	E	E	E	E	E	T	T	E	E	E	E	E	T	E
241	E	E	T	T	T	E	C	C	T	C	E	E	E	E	E	E	E	E	T	T	C	E	E	E	E	E
271	C	C	C	E	E	E	E	H	H	E	E	E	E	E	E	E	C	C	E	E	E	E	E	E	E	E
301	H	H	H	H	H	H	E	T	T	C	C	C	T	E	T	T	E	T	E	E	E	E	E	E	E	E
331	E	E	E	C	E	C	H	H	H	H	E	E	E	E	C	C	C	C	E	E	E	E	E	E	E	E
361	E	E	E	E	E	E	E	E	E	E	E	E	E	E	C	C	C	T	E	E	E	T	C	C	T	C
391	C	H	H	H	E	E	E	H	H	H	H	C	C	C	T	T	C	C	C	T	E	E	E	E	E	C
421	H	H	H	H	H	H	H	C	C	C	H	H	H	H	H	H	H	H	H	H	H	E	E	E	E	E
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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FIGURE 14-3

451 E E C S E E T T E E E E E E E E E E H H H H H H H H H H
481 H C S H H H H H H H H H H T T T C C C T E E E E E E
511 E E E E C C C C E E E E H H H H H H T C C C E E T E C T
541 T E T T T T C E E E E E E E E E E H H H H H H T H H H
571 H H H H H H E E E E E E E E E E H H H H H H T H H H
601 H H H H H H H H H H H H E E E E E E H H H H H H E E E E
631 H H H H H H H H H H H H H H H H H T T C C E E E E E E
661 E E E H H H H H H H H H H H H E E T T C C T E E E E E E
691 E E E T C C C C T E E E E E E E E E E H H H H H H H C C
721 C H

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FIGURE 14-4

Semi-graphical output.

=====

Symbols used in the semi-graphical representation:

Helical conformation: X	Extended conformation: -
Turn conformation: >	Coil conformation: *

10	20	30	40	50
MWNLLHETDS	AVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEAT			
XXXXXXXXXXXXXX	----->	XXXXXXXXXXXXXX	----->	XXXXXXXXXXXXXX
XXXXXXXXXXXXXX	----->	XXXXXXXXXXXXXX	----->	XXXXXXXXXXXXXX
60	70	80	90	100
NITPKHNMKAFLDELKAENIKKFLYNFTQIPHLAGTEQNFLAKQIQSQW				

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FIGURE 14-5

```

XXXXXXXXXXXXXXXXXXXX-->>-----XXXXXXXXXXXXX-X*--
XXXXXXXXXXXXXXXXXXXX-->>-----XXXXXXXXXXXXX-X*--

110      120      130      140      150
|         |         |         |         |
KEFGLDSVELAHYDVLLSYPNKTHPNYISINEDGNEIFNTSLFEPPPPG

->>*****-->>>>*****-->>*****-->>*****>
->>*****-->>>>*****-->>*****-->>*****>

160      170      180      190      200
|         |         |         |         |
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI

```


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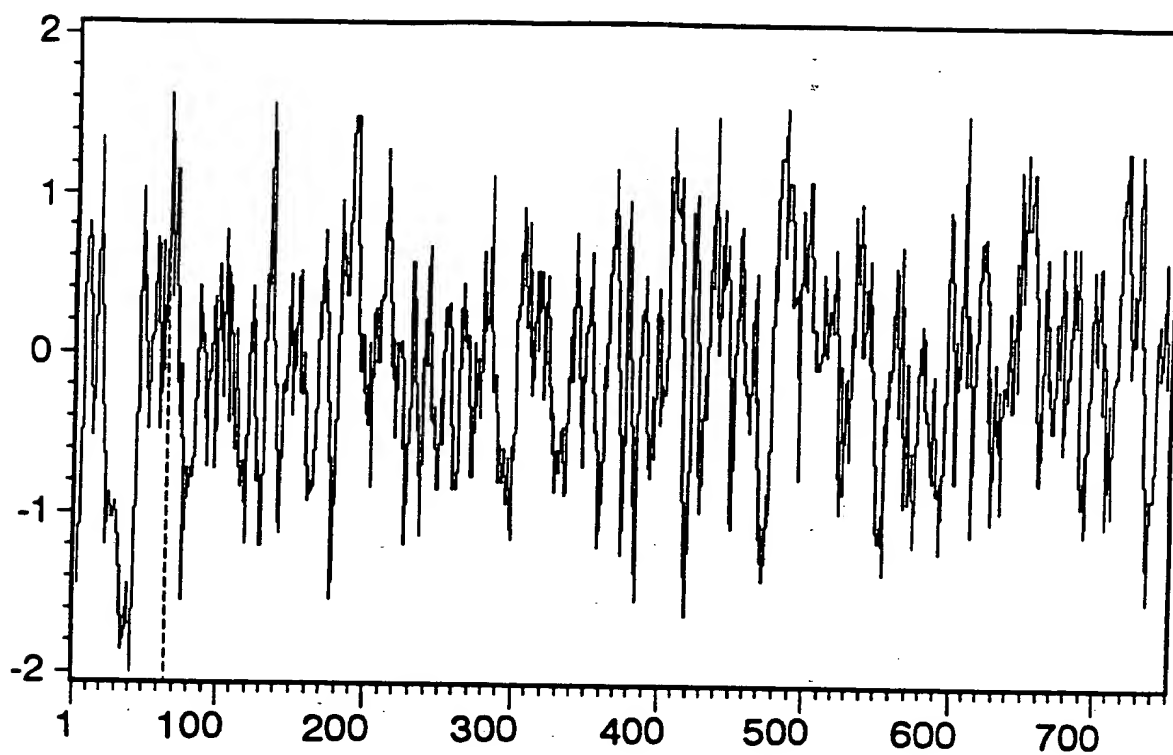
FIGURE 14-8

LYHSVYETVELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY
 -----XXXXXXXXXXXXX-X-----XXXXXXXX----->XXX
 -----XXXXXXXXXXXXX-X-----XXXXXXXX----->XXX
 610 620 630 640 650
 | | | | |
 AVVLRKYADKIYSISMKHPQEMKTYSVSFDLSFAVKNFTEIAKFSERL
 XXXXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX
 XXXXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX
 660 670 680 690 700
 | | | | |
 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY
 XX>>>*>-----XXXXXXXXXX-->>***>----->***>
 XX>>>*>-----XXXXXXXXXX-->>***>----->***>
 710 720 730 740 750
 | | | | |
 AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAETLSEVA
 ----->-----XXXXXXXXXX----->-----XXXXXXXXXXXXXXXXXX
 ----->-----XXXXXXXXXX----->-----XXXXXXXXXXXXXXXXXX

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FIGURE 15A



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FIGURE 15B

 * PREDICTION OF ANTIGENIC DETERMINANTS *

Done on sequence PMSANTIGEN.

Total number of residues is: 750.

Analysis done on the complete sequence.

The method used is that of Hopp and Woods.

The averaging group length is: 6 amino acids.

-> This is the value recommended by the authors <-

The three highest points of hydrophilicity are:

(1)	Ah= 1.62 :	From 63 to 68 :	Asp-Glu-Leu-Lys-Ala-Glu
(2)	Ah= 1.57 :	From 132 to 137 :	Asn-Glu-Asp-Gly-Asn-Glu
(3)	Ah= 1.55 :	From 482 to 487 :	Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third point: gave a proportion of 33% of incorrect predictions.

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FIGURE 16-3

	1440	1450	1460	1470	1480	1490
pmsgen	AGCTGTTGTT	CATGAAAT	TGTGAG---	GAGCTTTGGA	CACTGAA	AAAGGAAGG
	1390	1400	1410	1420	1430	1440
CHKTFE	TGCTATATTG	TGGAACTT	GCCCCGTG	TGATCTCAG	ACATAGTGA	AAACGAGG

	1500	1510	1520	1530	1540	1550
pmsgen	ACCTAGAAGAACAAATTTTGTTC	CAAGCTGGGATGCAGAGAAATTT	GGCTCTTCTTGCTTC	GGTTC		
	::: ::	::: ::	X::: ::	::: ::	::: ::	::: ::
CHKTFE	ACCGAGCGGAAGCATCTTTGCT	AGCTGGAGTGCAGGAGACTACG	GAGCTGTGGGTGC			
	1450	1460	1470	1480	1490	1500

	1560	1570	1580	1590	1600	1610
pmsgen	TACTGAGTGGCAGAGGAGAA	TTCAAGACTCCTTCAAGAGCGTG	GGCTTATATA	TAA		
	::::: ::	::::: : : : X	: : : : :	: : : : :	: : : : :	: : : : :
CHKTFE	TACTGAATGGCTGGAGGGTACT	CTGCCATGCTGCATGCCAAAGCTT	CACCTACATCA-			
	1510	1520	1530	1540	1550	1560

	1620	1630	1640	1650	1660	1670
pmsgen	TGC-TGACTCATCTATAGAGGAACTA-CACTCTGAGAGTTGATTGTACACCGCTGATG					
	:: :: : :: :	:: :: :	:: :: :	:: :: :	:: :: :	:: :: :
CHKTFE	-GCTTGGATGCTCCAGTCCCTGGGAGCAAGCCCATGTCAAGATTCTGCCAGCCCCCTTGCTG					
	1570	1580	1590	1600	1610	1620

FIGURE 16-5

RATRRR Rat transferrin receptor mRNA, 3' end. 164 164 311
 55.5% identity in 560 nt overlap

1210 1220 1230 1240 1250
 pmsgen CCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAAATGTTGGACCTGGCTT-

1260 1270 1280 1290 1300 1310
 pmsgen -TACTGGAAACTTTTCTACACAAAGTCAAGATGCACATC-CACTCT-ACCAATG----

RATRRF TGCAGAAAGCTATTCAAAAACATGGGAAGGAAACTGTCCCTAGTTGGAATATAGATTC
 610 620 630 640 650 660

RATRRF CTCATGTAAGCTGGAACTTTCACAGAAATCAAAATGTGAAGCTCACTGTGAACAAATGTACT
 670 680 690 700 710 720

FIGURE 16-7

1550 1560 1570 1580 1590 1600
 pmsgen CTTGGTTCTACTGAGTGGGCAGAGAGAA---TTCAAGACTCCTTCAAGAGCGTGGCGTG
 : : : : : X : : : : : : :
 RATRF GTTGGTCCGACTGAGTGGCTGGAGGGGTACCTTTCATCTTTGCATCTAAAG---GCTTTC
 970 980 990 1000 1010 1020
 1610 1620 1630 1640 1650 1660
 pmsgen GCTTATATTAATGCTGACTCATCTATAGAAGGAACTA-CACTCTGAGAGTTGATTGTAC
 : : : : : : : : : : : : : : : :
 RATRF ACTTACATTAAAT-CTGGATAAAGTCGTCCTGGGTACTAGCAACTTCAAGGTTTCTGCCAG
 1030 1040 1050 1060 1070 1080
 1670 1680 1690 1700 1710 1720
 pmsgen ACCGCTGATGTACAGCTTGGTACACACCTAACAAAGAGCTGAAAGC-CCTGATGAAG
 : : : : : : : : : : : : : : : :
 RATRF CCCCCATTATATACACTTATGGGGAAGATAATGCAGGA--CGTAAAGCATCCGA-----
 1090 1100 1110 1120 1130

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FIGURE 16-9

HUMTFR Human transferrin receptor mRNA, complete cd 145 145 266
54.3% identity in 464 nt overlap

```

1230      1240      1250      1260      1270
pmsgen AGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTAC--TGGAAACTTTTCTACAC
          : : : : : : : : : : : : : : : : : : : : : :
HUMTFR TATGGAAGGAGACTGTCCCTCTGACTGGAAACAGACTCTACATGTAGGATGGTAACCTC
1140      1150      1160      1170      1180      1190

```

```

1280      1290      1300      1310      1320      1330
pmsgen AAAAAGTCAAGATGCACATC-CACTCT-ACCAATG-----AAGTGACAAGAAATTACAA
          : : : : : : : : : : : : : : : : : : : : : :
HUMTFR AGAAAGCAAGAATGTGAAGCTCACTGTGAGCAATGTGCTGAAAGAGATAAAATTCTTAA
1200      1210      1220      1230      1240      1250

```

```

1340      1350      1360      1370      1380      1390
pmsgen TGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAAGACAGATATGTCATTCTGGGAGGTCA
          : : : : : : : : : : : : : : : : : : : : : :
HUMTFR CATCTTTGGAGTTATTAAAGGCTTTGTAGAACCAAGATCACTATGTGTAGTTGGGGCCCA
1260      1270      1280      1290      1300      1310

```

```

1400      1410      1420      1430      1440      1450
pmsgen CCGGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAGAGT-GGAGCAGCTGTTGTTTCATG
          : : : : : : : : : : : : : : : : : : : : : :
HUMTFR GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA
1320      1330      1340      1350      1360      1370

```


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FIGURE 16-10

1460	1470	1480	1490	1500
pmsgen	AAATTG---	TGAGGAGCTTTGGAACTGAA	AAAGGAAGGTGGAGACCTAG	AAGACAA
	:: ::	:: ::	:: ::	:: ::
HUMTFR	AACTTGCCAGATGTTCTCAGATATGGTCTTAA	AAGATGGGTTTCAGCCCAGCAGAA	GCA	
1380	1390	1400	1410	1420
1510	1520	1530	1540	1550
pmsgen	TTTTGTTGCAAGCTGGGATGCAGAA	GAATTTGGTCTTCTTGTTCTACTGAGTGGCAG		
	:: ::	:: ::	:: ::	:: ::
HUMTFR	TTATCTTTGCCAGTTGGAGTGTGGACTTTGGATCGGTTGGTGCCACTGAATGGCTAG			
1440	1450	1460	1470	1480
1570	1580	1590	1600	1610
pmsgen	A-GGAGAA	TTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCT		
	:: ::	:: ::	:: ::	:: ::
HUMTFR	AGGGATACCTTTTCGTC-CCTGCATTTAAAGGCTTTCACTTATATTAATCTGGATAAAGCG			
1500	1510	1520	1530	1540
1630	1640	1650	1660	1670
pmsgen	ATAGAAGGA	AACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACA-GCTTGGT-AC		
	:: ::	:: ::	:: ::	:: ::
HUMTFR	GTTCTTGGTACCAGCAACTTCAAGGTTTCTGCCAGCCCACTGTTGTATACGCTTATTGAG			
1560	1570	1580	1590	1600

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FIGURE 16-11

1690	1700	1710	1720	1730	1740
pmsgen	ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAA	TCTCTTATG			
:	:	:	:	:	:
HUMTFR	AAAACAATGCACAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC				
1620	1630	1640	1650	1660	1670

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FIGURE 17A



FIGURE 17B

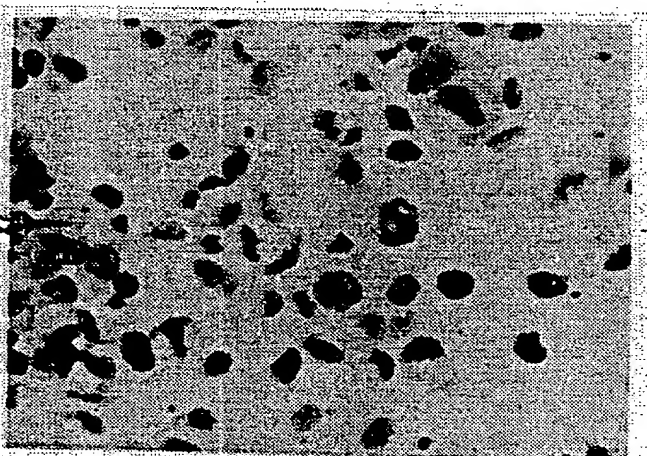
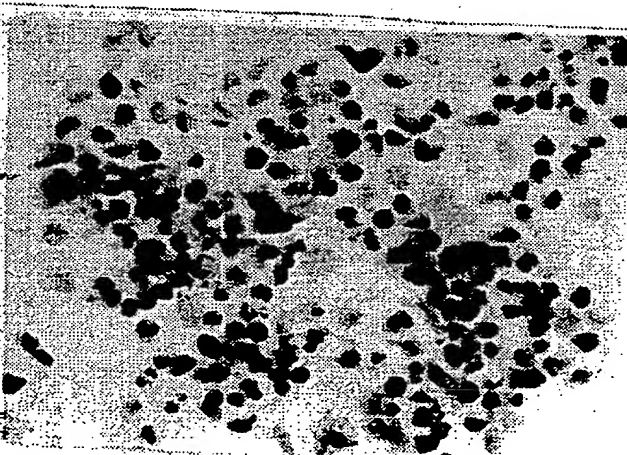


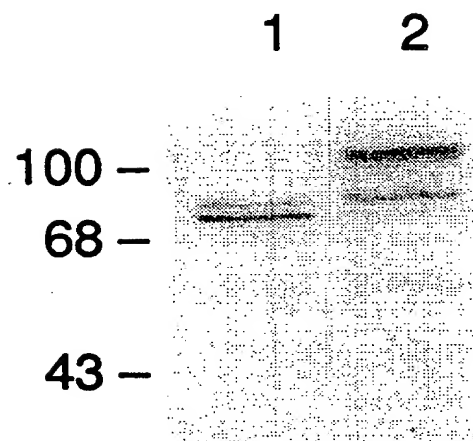
FIGURE 17C



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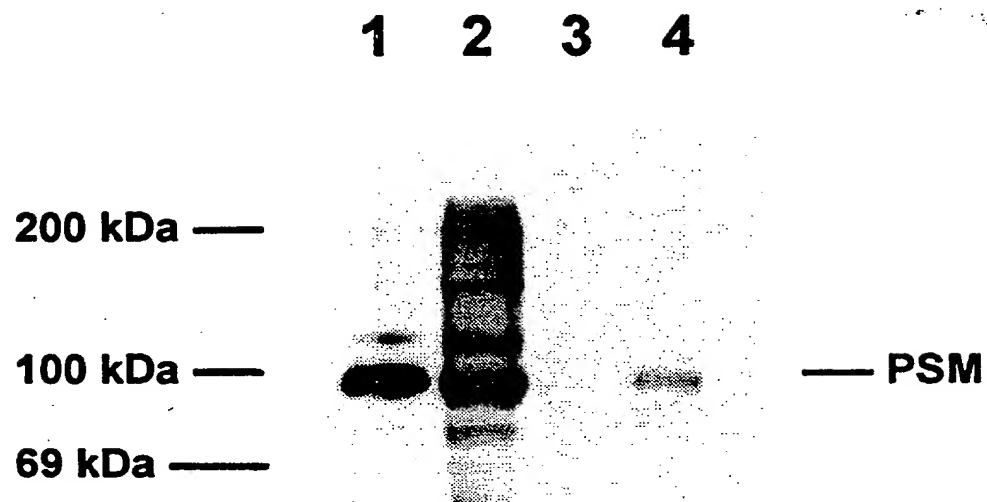
FIGURE 18



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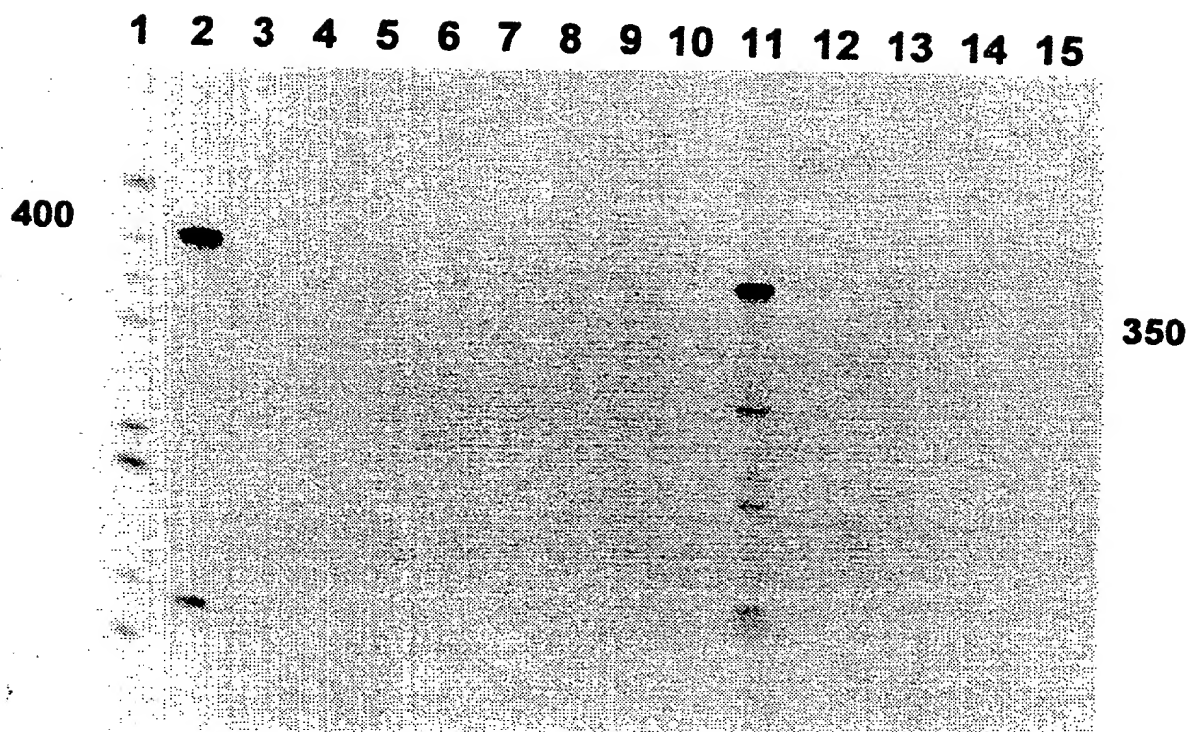
FIGURE 19



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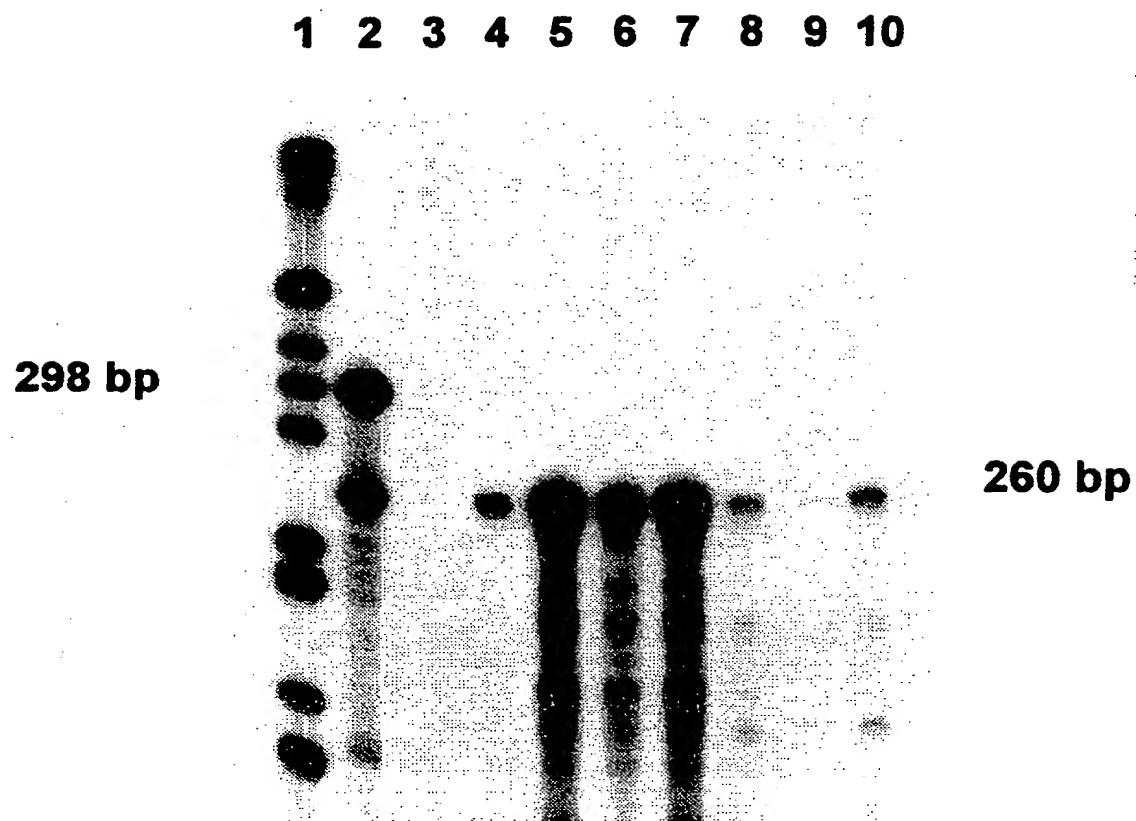
FIGURE 20



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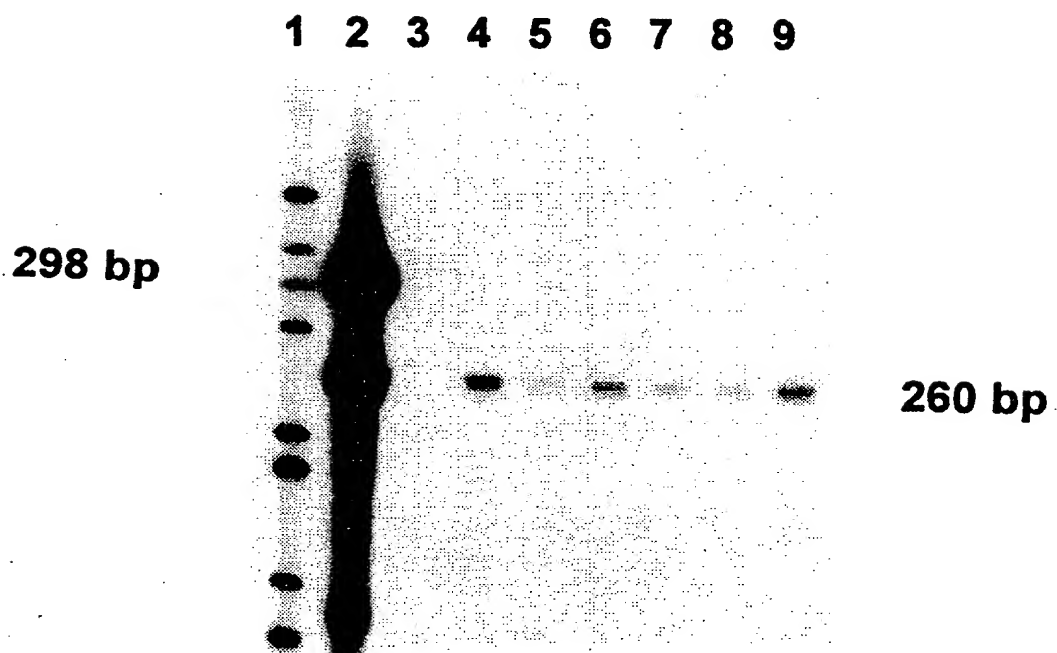
FIGURE 21



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FIGURE 22



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FIGURE 23

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CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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FIGURE 24A

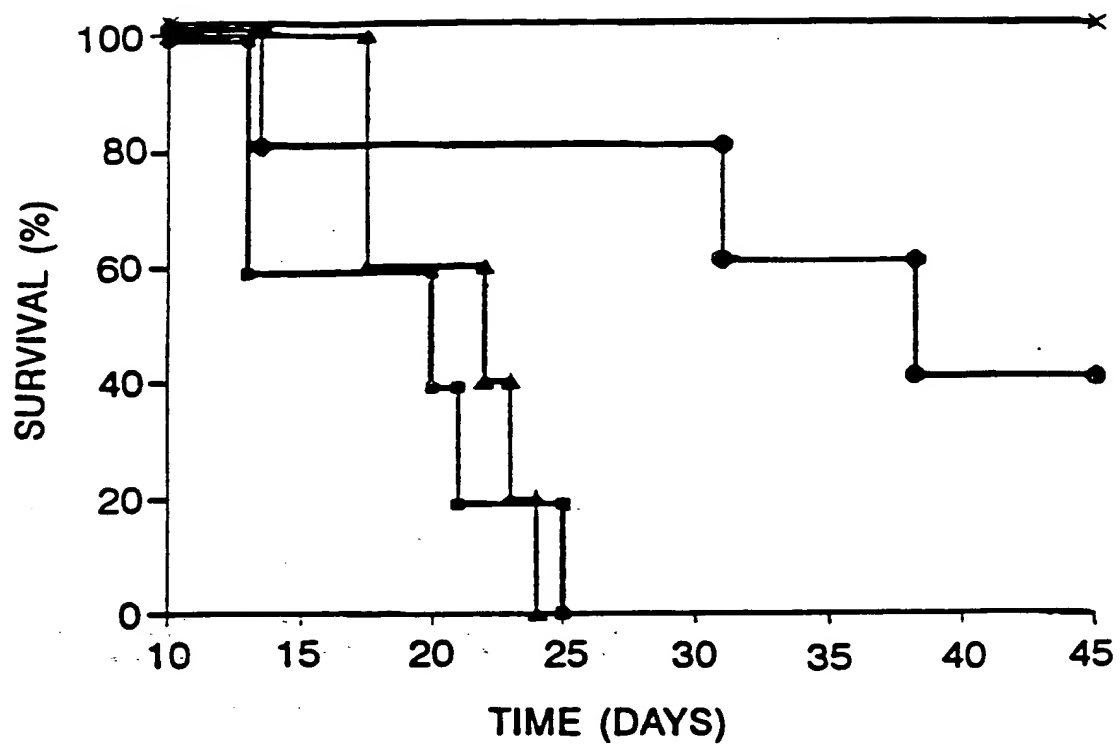
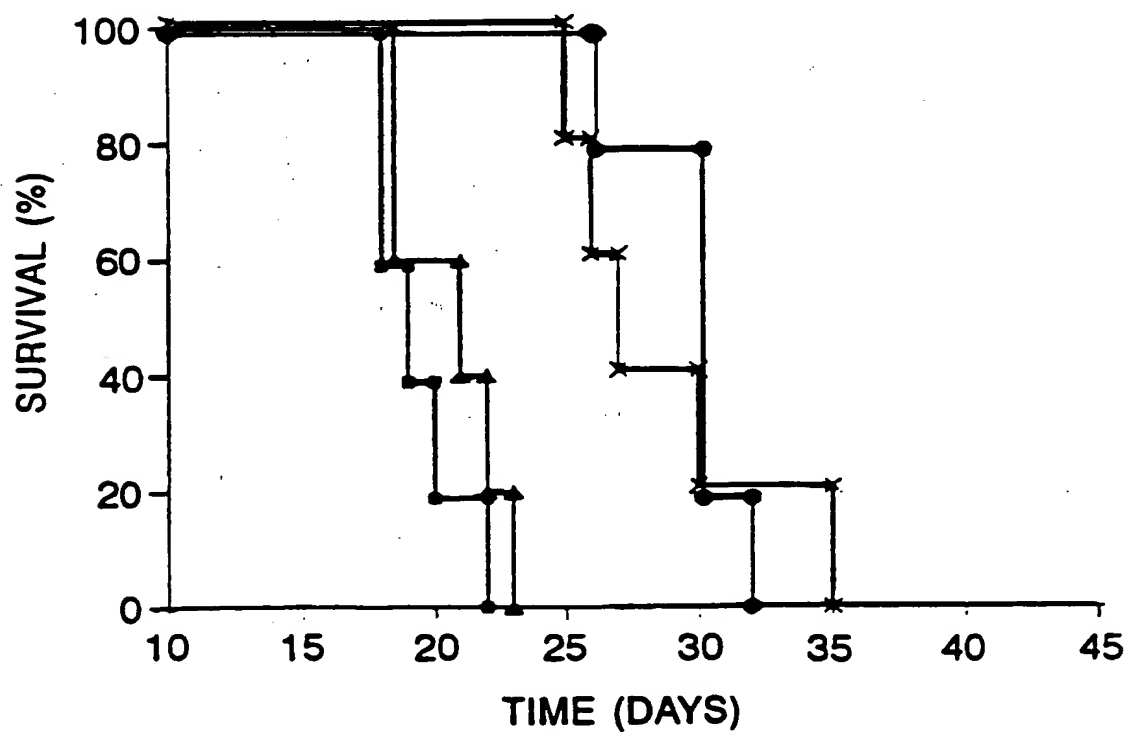


FIGURE 24B



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FIGURE 25A

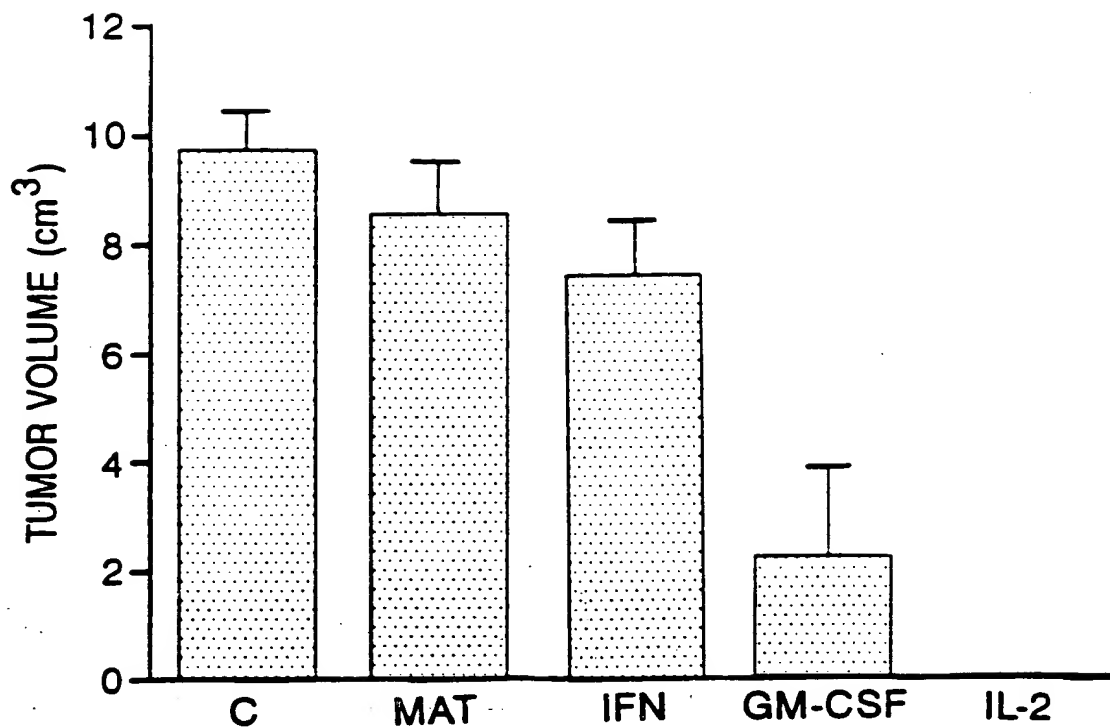
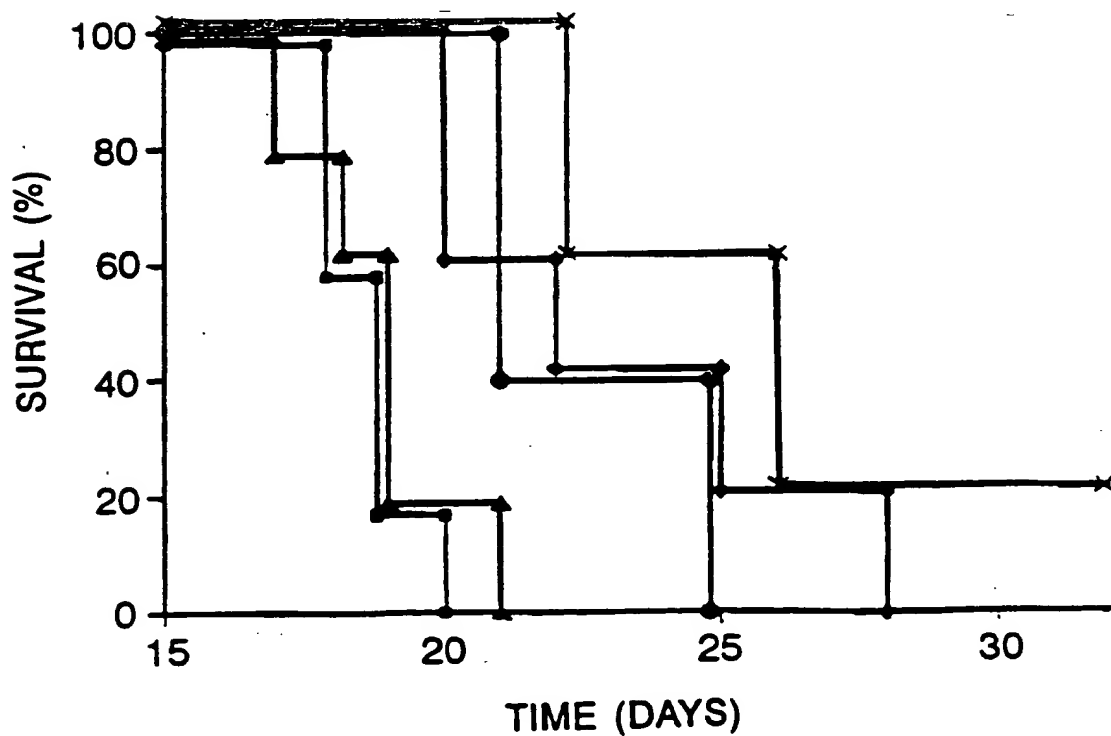


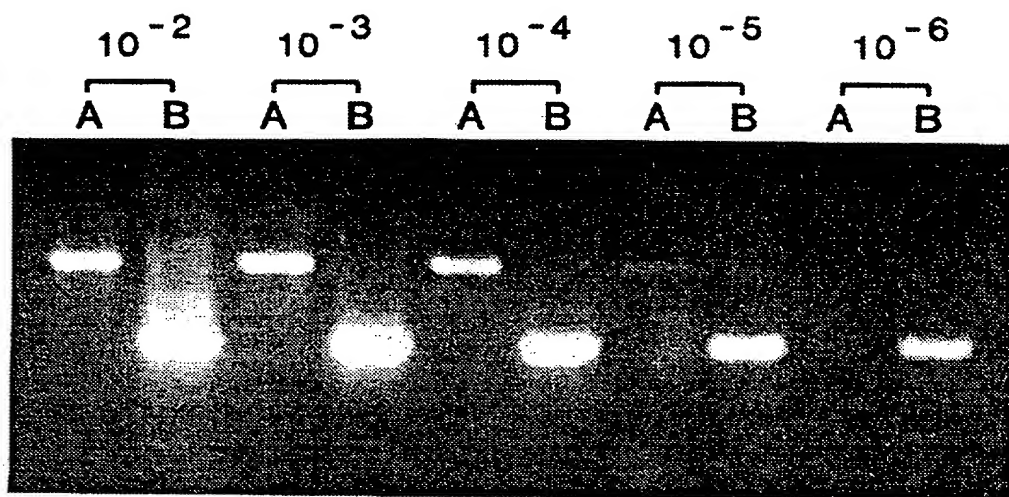
FIGURE 25B



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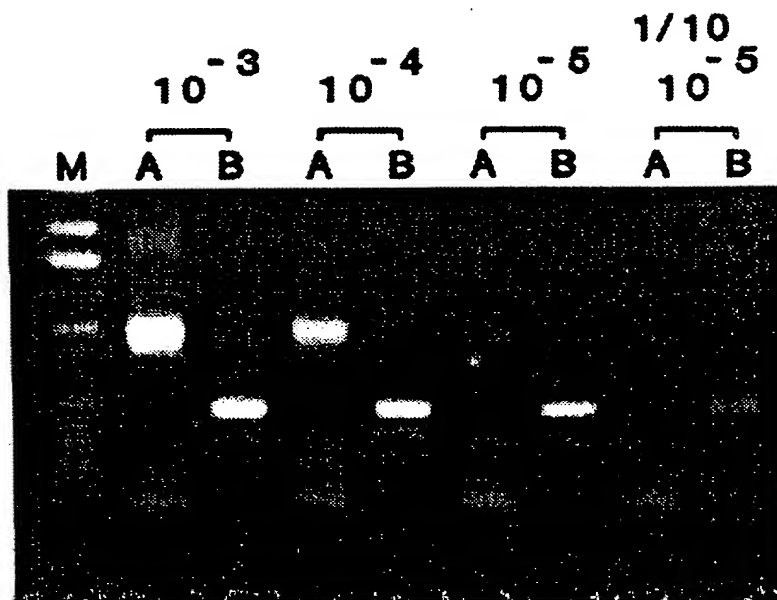
FIGURE 26



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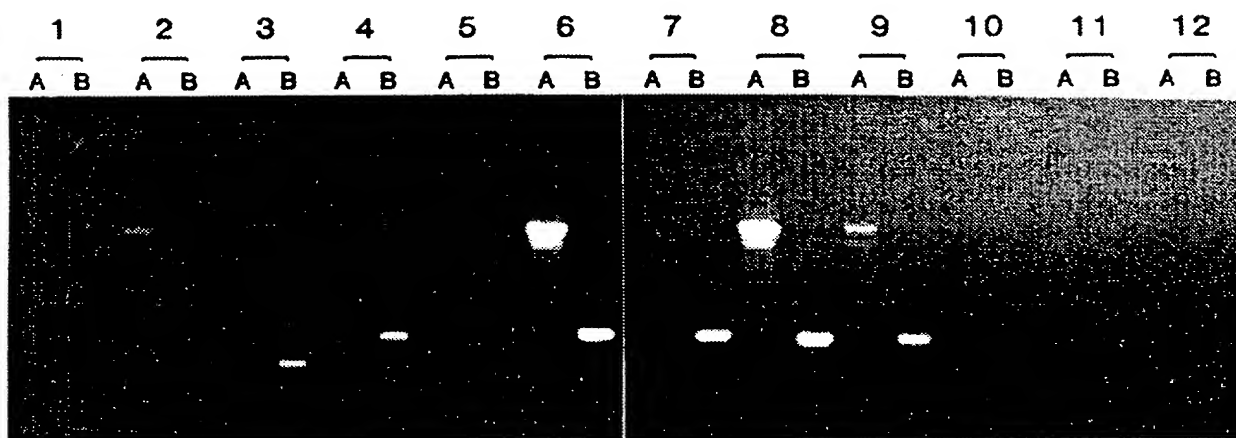
FIGURE 27



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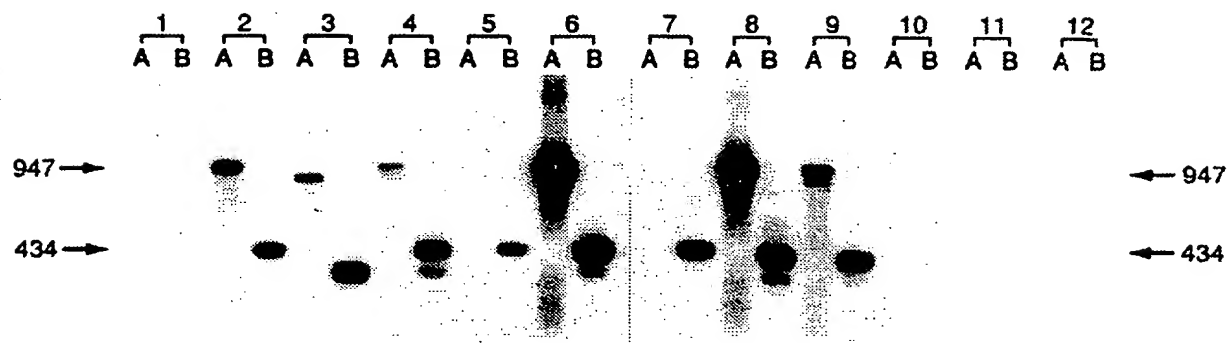
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FIGURE 28



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FIGURE 29



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FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-

SUBSTITUTE SHEET (RULE 26)